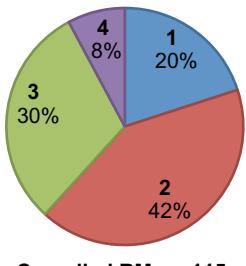
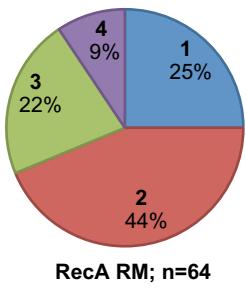
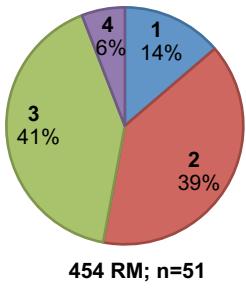
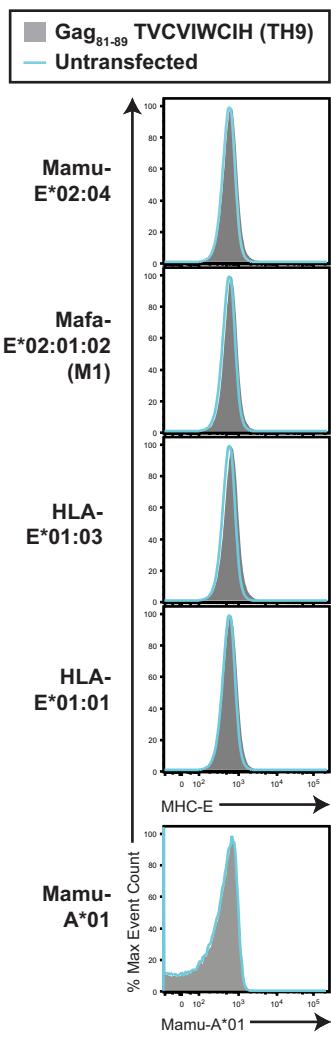


**Supplemental Figure 1. MHC-E alleles of humans, rhesus macaques, and Mauritius cynomolgus macaques.** Amino acid alignment of the  $\alpha 1$  and  $\alpha 2$  regions of 33 Mamu-E, 4 Mafa-E, and 2 HLA-E alleles. Novel alleles are indicated in bold. B and F pocket residues predicted to contact peptide (58, 59) are highlighted in blue and red, respectively. Note that B and F pocket residues are conserved among all MHC-E molecules, with the exception of 3 Mamu-E alleles (Mamu-E\*02:15, -E\*02:20, and -E\*02:30) and 1 Mafa-E allele (Mafa-E\*02:14).

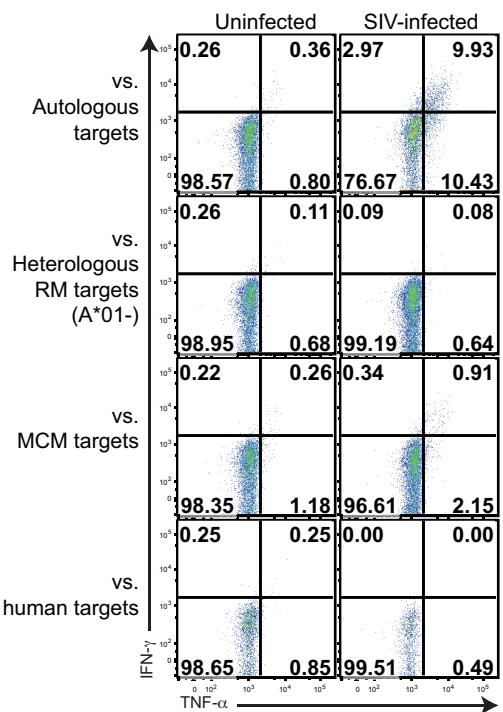


**Supplemental Figure 2. Individual rhesus macaques express between 1 and 4 Mamu-E molecules.** Pie charts summarizing the number of distinct MHC-E transcripts sequenced from individual rhesus macaques via 454 deep sequencing of 190-bp amplicons of MHC-I (top panel, n=51) or RecA capture of MHC-I cDNAs and subsequent Sanger sequencing (49) (middle panel, n=64). Compiled data representing 115 individual rhesus macaques is shown in the bottom panel.



### Supplemental Figure 3. Gag<sub>81-89</sub>(TH9) fails to stabilize surface MHC-E or Mamu-A\*01 expression.

Representative histogram overlays of MHC-E (top) or Mamu-A\*01 (bottom) surface staining of 293T cells on untransfected cells (blue) and cells transfected with single chain trimer constructs encoding negative control peptide Gag<sub>81-89</sub>(TH9) (gray). Histograms show live cells.



**Supplemental Figure 4. SIV-specific, Mamu-A\*01-restricted CD8+ T cells cannot recognize SIV-infected CD4+ T cells derived from other primate species.** Representative flow cytometric ICS plots showing recognition of autologous and heterologous SIV-infected CD4+ T cell targets by an SIVgag<sub>181-189</sub>(CM9)-specific CD8+ T cell line (Mamu-A\*01-restricted). Plots are gated on live, CD3+, CD8+, CD4- cells.